



## Blast 2 Sequences results

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### BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.1.2 [Nov-13-2000]

Match:  Mismatch:  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:   Filter  Align

Sequence 1 lcl|seq\_1 Length 137 (1 .. 137)

Sequence 2 lcl|seq\_2 Length 612 (1 .. 612)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 148 bits (77), Expect = 5e-34  
Identities = 81/83 (97%)  
Strand = Plus / Minus

Query: 1 ccggtaagtaaacagtcagaaaattagcatgaaaggcagttagcattggaggaagcaca 60  
Sbjct: 85 ccggtaagtaaacagtcagaaaattagcatgaaaggcagttagcattggaggaagctca 26

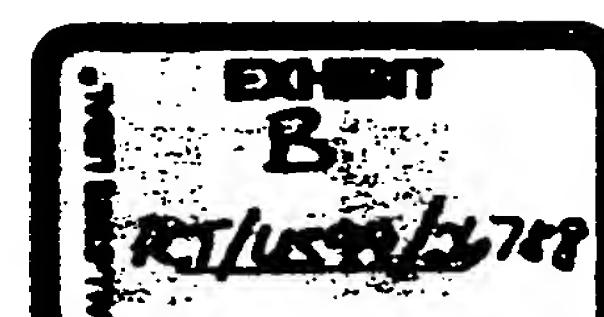
Query: 61 gatctctagagctgtccgtcg 83  
Sbjct: 25 gatctctagagctgtccgtcg 3

CPU time: 0.02 user secs. 0.06 sys. secs 0.08 total secs.

Gapped  
Lambda K H  
1.33 0.621 1.12

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Lambda K H  
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Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 1  
Number of Sequences: 0  
Number of extensions: 1  
Number of successful extensions: 1



Number of sequences better than 10.0: 1  
length of query: 157  
length of database: 2,635,864,967  
effective HSP length: 22  
effective length of query: 115  
effective length of database: 2,635,864,945  
effective search space: 303124468675  
effective search space used: 303124468675  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 18 (35.3 bits)